

VED
AUG 29 2000
TECH CENTER 1600/2900

1646

PH#13

RAW SEQUENCE LISTING DATE: 08/18/2000
PATENT APPLICATION: US/09/401,839 TIME: 13:37:45

Input Set : A:\1803247
Output Set: N:\CRF3\08182000\I401839.raw

ENTERED

4 <110> APPLICANT: Gately et al.
6 <120> TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC
7 LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
8 ANTIBODIES THERETO
10 <130> FILE REFERENCE: 1803-247
12 <140> CURRENT APPLICATION NUMBER: 09/401,839
13 <141> CURRENT FILING DATE: 1999-09-22
15 <160> NUMBER OF SEQ ID NOS: 34
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 306
21 <212> TYPE: PRT
22 <213> ORGANISM: Homo sapiens
24 <400> SEQUENCE: 1
25 Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp Tyr
26 1 5 10 15
27 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro Glu
28 20 25 30
29 Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu Gly
30 35 40 45
31 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
32 50 55 60
33 Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu Leu
34 65 70 75 80
35 Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
36 85 90 95
37 Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala Lys
38 100 105 110
39 Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser Thr
40 115 120 125
41 Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln
42 130 135 140
43 Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg Gly
44 145 150 155 160
45 Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser Ala
46 165 170 175
47 Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp Ala
48 180 185 190
49 Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg
50 195 200 205
51 Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro Leu
52 210 215 220
53 Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp
54 225 230 235 240
55 Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val Gln
56 245 250 255
57 Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys Thr

see p. 5

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```

58          260          265          270
59 Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg Ala
60          275          280          285
61 Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val Pro
62          290          295          300
63 Cys Ser
64 305
66 <210> SEQ ID NO: 2
67 <211> LENGTH: 1397
68 <212> TYPE: DNA
69 <213> ORGANISM: Homo sapiens
71 <220> FEATURE:
72 <221> NAME/KEY: CDS /
73 <222> LOCATION: (41)...(1024)
75 <400> SEQUENCE: 2
76 gtttcagggc cattggactc tccgtcctgc ccagagcaag atg tgt cac cag cag 55
77          Met Cys His Gln Gln
78          1          5
80 ttg gtc atc tct tgg ttt tcc ctg gtt ttt ctg gca tct ccc ctc gtg 103
81 Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu Ala Ser Pro Leu Val
82          10          15          20
84 gcc ata tgg gaa ctg aag aaa gat gtt tat gtc gta gaa ttg gat tgg 151
85 Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val Val Glu Leu Asp Trp
86          25          30          35
88 tat ccg gat gcc cct gga gaa atg gtg gtc ctc acc tgt gac acc cct 199
89 Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asp Thr Pro
90          40          45          50
92 gaa gaa gat ggt atc acc tgg acc ttg gac cag agc agt gag gtc tta 247
93 Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln Ser Ser Glu Val Leu
94          55          60          65
96 ggc tct ggc aaa acc ctg acc atc caa gtc aaa gag ttt gga gat gct 295
97 Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala
98          70          75          80          85
100 ggc cag tac acc tgt cac aaa gga ggc gag gtt cta agc cat tcg ctc 343
101 Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Leu
102          90          95          100
104 ctg ctg ctt cac aaa aag gaa gat gga att tgg tcc act gat att tta 391
105 Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu
106          105          110          115
108 aag gac cag aaa gaa ccc aaa aat aag acc ttt cta aga tgc gag gcc 439
109 Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe Leu Arg Cys Glu Ala
110          120          125          130
112 aag aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg aca atc agt 487
113 Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Thr Ile Ser
114          135          140          145
116 act gat ttg aca ttc agt gtc aaa agc agc aga ggc tct tct gac ccc 535
117 Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg Gly Ser Ser Asp Pro
118          150          155          160          165
120 caa ggg gtg acg tgc gga gct gct aca ctc tct gca gag aga gtc aga 583

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```

121 Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Arg Val Arg
122      170      175      180
124 ggg gac aaa caa gga tat gag tac tca gtg gag tgc cag gag gac agt      631
125 Gly Asp Lys Gln Gly Tyr Glu Tyr Ser Val Glu Cys Gln Glu Asp Ser
126      185      190      195
128 gcc tgc cca gct gct gag gag agt ctg ccc att gag gtc atg gtg gat      679
129 Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Met Val Asp
130      200      205      210
132 gcc gtt cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc      727
133 Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
134      215      220      225
136 agg gac atc atc aaa cct gac cca ccc aag aac ttg cag ctg aag cca      775
137 Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro
138      230      235      240      245
140 tta aag aat tct cgg cag gtg gag gtc agc tgg gag tac cct gac acc      823
141 Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
142      250      255      260
144 tgg agt act cca cat tcc tac ttc tcc ctg aca ttc tgc gtt cag gtc      871
145 Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Val Gln Val
146      265      270      275
148 cag ggc aag agc aag aga gaa aag aaa gat aga gtc ttc acg gac aag      919
149 Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg Val Phe Thr Asp Lys
150      280      285      290
152 acc tca gcc acg gtc atc tgc cgc aaa aat gcc agc att agc gtg cgg      967
153 Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala Ser Ile Ser Val Arg
154      295      300      305
156 gcc cag gac cgc tac tat agc tca tct tgg agc gaa tgg gca tct gtg      1015
157 Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Glu Trp Ala Ser Val
158      310      315      320      325
160 ccc tgc agt taggttctga tccaggatga aaatttggag gaaaagtgga      1064
161 Pro Cys Ser
164 agatattaag caaaatgttt aaagacacaa cggaatagac ccaaaaagat aatttctatc      1124
165 tgatttgctt taaaacgttt ttttaggac acaatgatat ctttgctgta tttgtatagt      1184
166 tagatgctaa atgctcattg aaacaatcag ctaattttatg tatagatttt ccagctctca      1244
167 agttgccatg ggccttcacg ctattttaa atttaagtaa tttatgtatt tattagtata      1304
168 ttactgttat ttaacgtttg tctgccagga tgtatggaat gtttcatact cttatgacct      1364
169 gatccatcag gatcagtcct tattatgcaa aat      1397
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 328
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 3
177 Met Cys His Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Phe Leu
178      1      5      10      15
179 Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
180      20      25      30
181 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
182      35      40      45
183 Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln

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```

184          50          55          60
185 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
186 65          70          75          80
187 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
188          85          90          95
189 Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
190          100         105         110
191 Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
192          115         120         125
193 Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
194          130         135         140
195 Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
196 145         150         155         160
197 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
198          165         170         175
199 Ala Glu Arg Val Arg Gly Asp Lys Gln Gly Tyr Glu Tyr Ser Val Glu
200          180         185         190
201 Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
202          195         200         205
203 Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
204          210         215         220
205 Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
206 225         230         235         240
207 Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
208          245         250         255
209 Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
210          260         265         270
211 Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
212          275         280         285
213 Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
214          290         295         300
215 Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
216 305         310         315         320
217 Glu Trp Ala Ser Val Pro Cys Ser
218          325
220 <210> SEQ ID NO: 4
221 <211> LENGTH: 856
222 <212> TYPE: DNA
223 <213> ORGANISM: Homo sapiens
225 <220> FEATURE:
226 <221> NAME/KEY: CDS /
227 <222> LOCATION: (170)...(826)
229 <400> SEQUENCE: 4
230 gaattcccag aaagcaagag accagagtcc cgggaaagtc ctgccgcgcc tcgggacaat      60
231 tataaaaatg tggcccccctg ggtcagcctc ccagccaccg ccctcacctg ccgcggccac      120
232 aggtctgcat ccagcggctc gccctgtgtc cctgcagtgc cggctcagc atg tgt cca      178
233                                     Met Cys Pro
234                                     1
236 gcg cgc agc ctc ctc ctt gtg gct acc ctg gtc ctc ctg gac cac ctc      226

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```

237 .Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu Asp His Leu
238      5      10      15
240 agt ttg gcc aga aac ctc ccc gtg gcc act cca gac cca gga atg ttc      274
241 Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro Gly Met Phe
242      20      25      30      35
244 cca tgc ctt cac cac tcc caa aac ctg ctg agg gcc gtc agc aac atg      322
245 Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Met
246      40      45      50
248 ctc cag aag gcc aga caa act cta gaa ttt tac cct tgc act tct gaa      370
249 Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys Thr Ser Glu
250      55      60      65
252 gag att gat cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag      418
253 Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu
254      70      75      80
256 gcc tgt tta cca ttg gaa tta acc aag aat gag agt tgc cta aat tcc      466
257 Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys Leu Asn Ser
258      85      90      95
260 aga gag acc tct ttc ata act aat ggg agt tgc ctg gcc tcc aga aag      514
261 Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys
262      100      105      110      115
264 acc tct ttt atg atg gcc ctg tgc ctt agt agt att tat gaa gac ttg      562
265 Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu
266      120      125      130
268 aag atg tac cag gtg gag ttc aag acc atg aat gca aag ctt ctg atg      610
269 Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys Leu Leu Met
270      135      140      145
272 gat cct aag agg cag atc ttt cta gat caa aac atg ctg gca gtt att      658
273 Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Ala Val Ile
274      150      155      160
276 gat gag ctg atg cag gcc ctg aat ttc aac agt gag act gtg cca caa      706
277 Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr Val Pro Gln
278      165      170      175
280 aaa tcc tcc ctt gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc      754
281 Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu
282      180      185      190      195
284 tgc ata ctt ctt cat gct ttc aga att cgg gca gtg act att gac aga      802
285 Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg
286      200      205      210
288 gtg acg agc tat ctg aat gct tcc taaaaagcga ggtccctcca aaccgttgtc      856
289 Val Thr Ser Tyr Leu Asn Ala Ser
290      215
293 <210> SEQ ID NO: 5
294 <211> LENGTH: 219
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <400> SEQUENCE: 5
299 Met Cys Pro Ala Arg Ser Leu Leu Leu Val Ala Thr Leu Val Leu Leu
300      1      5      10      15
301 Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Output Set: N:\CRF3\08182000\I401839.raw

L:351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:688 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31